ABSTRACT

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Anthelmintics are pharmaceuticals used in human and veterinary medicine for the treatment of infections caused by helminths. Although their benefits for treated organisms are undeniable, the impact on the ecosystem in general has not yet been thoroughly studied. Anthelmintics and their metabolites can reach the environment through different routes. Directly via an excretion into the faeces and urine of treated livestock animals or indirectly by an application of contaminated manure to soil or its seepage into surface water or groundwater. This exposure has significant and diverse impacts on non-target terrestrial or aquatic organisms and plants. Plants are able to uptake xenobiotics and detoxify them via various metabolic pathways. Phytoremediation as a method that utilizes plants for removing pollutants from environment is based on these pathways and can be effectively used for areas contaminated with anthelmintics.

The aim of this study was to obtain further information about changes in the proteome of model plant *Arabidopsis thaliana* after the exposure to four different types of anthelmintics (benzimidazoles fenbendazole and flubendazole, macrocyclic lactone ivermectin and aminoacetonitrile derivative monepantel) by two-dimensional polyacrylamide gel electrophoresis. Stress-related modifications in plant proteome were found. The differences were characterized by increased or decreased intensity of the spots on a protein maps and the final influence depended on exposure time.